

AATTGCCCCCT TCAGCTCCAA TTGCTCTATG TTTAGAAATTG CCTCTTTTTC AAGATGGATT 60  
TCCTTTCACAG GAATGGAGTG CTCATAATTC AGCATTTGCA GAAGGACTAC CGAGCTTACT 120  
ACACTTTTCT AAATTTTATG TCCAATGTTG GAGACCCACAG GAATATCTTT TTCAATTTATT 180  
TTCCACTTTG TTTTCAATTT AATCAGACAG TTGGAACCAA GATGATATGG GTAGCAGTCA 240  
TTGGGGATTG GTTAAATCTT ATATTTAAAT GGATATTATT TGGTCATCGA CCTTACTGGT 300  
GGGTCCAAGA AACTCAGATT TACCCAAATC ACTCAAGTCC ATGCCTTGAA CAGTTCCTA 360  
CTACATGTGA AACAGGTCCA GGAAGTCCAT CTGGCCATGC AATGGCGCA TCCTGTGTCT 420  
GGTATGTCAT GGTAAACCGCT GCCCTGAGCC AACTGTCTG TGGGATGGAT AAGTCTCTA 480  
TCACTCTGCA CAGACTGACC TGGTCATTTC TTTGGAGTGT TTTTGGTG ATTCAAATCA 540  
GTGCTGTCAT CTCAGAGTA TTCATAGCAA CACATTTTCC TCATCAAGTT ATTCTTGGAG 600  
TAATTGGTGG CATGCTGGTG GCAGAGGCCT TTGAACACAC TCCAGGCATC CAAACGGCCA 660  
GTCTGGGCAC ATACCTGAAG ACCAACCTCT TTCTCTTCTT GTTGCAGTT GGCTTTTACC 720  
TGCTTCTTAG GGTGCTCAAC ATTGACCTGC TGTGGTCCGT GCCCATAGCC AAAAAGTGGT 780  
GTGCTAACCC CGACTGGATC CACATTGACA CCACGCCCTT TGCTGGACTC GTGAGAAACC 840  
TTGGGGTCCCT CTTTGGCTTG GGCTTTGCAA TCAACTCAGA GATGTTCCTC CTGAGCTGCC 900  
GAGGGGAAA TAACTACACA CTGAGCTTCC GGTGCTCTG TGCCTTGACC TCATTGACAA 960  
TACTGCAGCT CTACCATTTT CTCCAGATCC CGACTCACGA AGAGCATTTA TTTTATGTGC 1020  
TGTCCTTTTG TAAAAGTGCA TCCATTCCCC TAACTGTGGT TGCTTTCATT CCCTACTCTG 1080  
TTCATATGTT AATGAACAA AGCGGAAAGA AGAGTCAGTA GAAAAAAA AAAA 1138

Fig. 1

Met Asp Phe Leu His Arg Asn Gly Val Leu Ile Ile Gln His Leu Gln  
1 5 10 15  
Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val  
20 25 30  
Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln  
35 40 45  
Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly  
50 55 60  
Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro  
65 70 75 80  
Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro  
85 90 95  
Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro  
100 105 110  
Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr  
115 120 125  
Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr  
130 135 140

Fig. 2A

Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile  
145 150 155 160

Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro  
165 170 175

His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala  
180 185 190

Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu  
195 200 205

Lys Thr Asn Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu  
210 215 220

Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys  
225 230 235 240

Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe  
245 250 255

Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala  
260 265 270

Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr  
275 280 285

Fig. 2B

Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu  
290 295 300

Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe  
305 310 315 320

Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val  
325 330 335

Ala Phe Ile Pro Tyr Ser Val His Met Leu Met Lys Gln Ser Gly Lys  
340 345 350

Lys Ser Gln  
355

Fig. 2C

```

H 1 MDFLHRNGVLI IQHLQKDYRAYYTFLENFMSNVGDPRNIFFIYFPLCFQFN
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
M 1 MDFLHRSGVLI IHHLQEDYRTYYGFLNFMSNVGDPRNIFSIYFPLWFQLN

H 51 QTVGTKMIWVAVIGDWLNLIFKWILFGHRPYWWVQETQIYPNHSSPCLEQ
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
M 51 QNVGTKMIWVAVIGDWFNLI FKWILFGHRPYWWIQETEIYPNHSSPCLEQ

H 101 FPTTCETGPGSPSGHAMGASCWVYVMVTAALSHTVCGMDKFSITLHRLTW
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
M 101 FPTTCETGPGSPSGHAMGSSCWVYVMVTAALSYTISRMEESSVTLHRLTW

H 151 SFLWSVFWLIQISVCISRVFIATHFPHQVILGVIGMLVAEAFEHTPGIQ
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
M 151 SFLWSVFWLIQISVCISRVFIATHFPHQVILGVIGMLVAEAFEHTPGVH

H 201 TASLGTYLKTNLFLFAVGFYLLLRVLNIDLLWSVPIAKKWCANPDWIIH
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
M 201 MASLSVYLKTNVFLFALGFYLLRLFGIDLWSVPIAKKWCANPDWIIH

H 251 IDTTPFAGLVRNLGVLFGGLGFAINSEMFLJSCRGNNYTLFRLLCALTS
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
M 251 IDSTPFAGLVRNLGVLFGGLGFAINSEMFLRSCQGENGTKPSFRLLCALTS

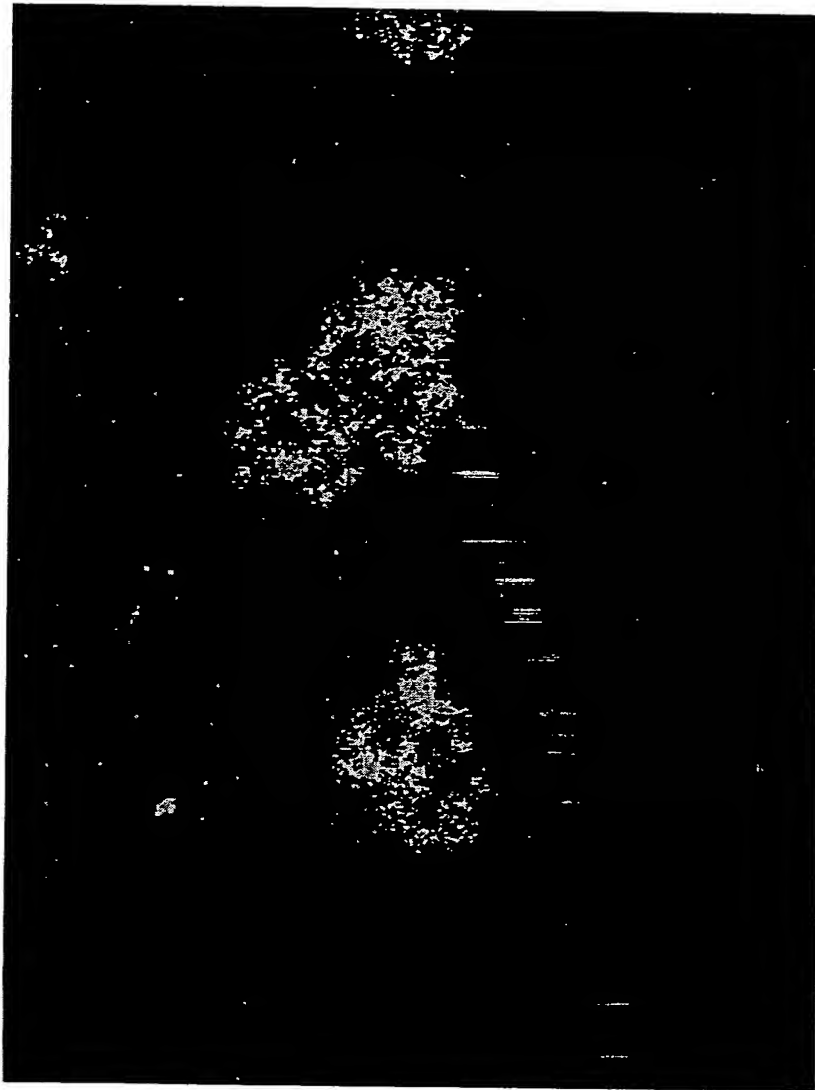
```

**Fig. 3A**

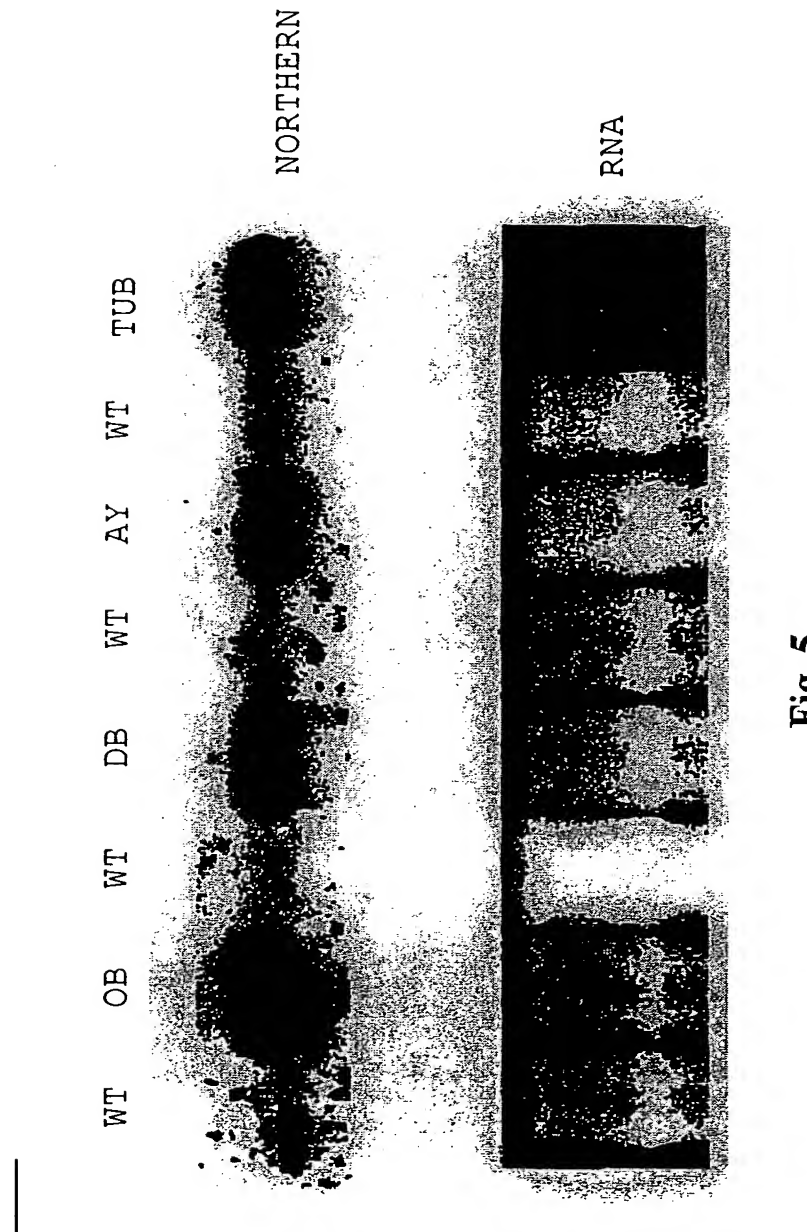
```
H 301 LTILQLYHFLQIPTHEEHLFYVLSFCKSASIPLTVAFIPYSVHMLMKQS
      || :||| |:.||| | |||.||||||| ||| ||| ||| | :
M 301 LTTMQLYRFIKIPTHAEPLFYLLSFCKSASIPLMVVALIPYCVHMLMRPG

H 351 GKKSQ
      ||..
M 351 DKKTK
```

Fig. 3B



**Fig. 4**





Hp MDFLHRNGVLI IQHLQKDYRAYYTFLNFMNSNVGDP RNIFFIYFPLCFQFN  
Mp MDFLHRSGVLI IHHLQEDYRTYYGFLN FMNSNVGDP RNIFFSIYFPLWFQLN  
F1 MDLLHSWGV ELAVYLQTRYGKYEG LFD LASTVADLHTTFFWLFP IWFHLR  
M1 MEEGMN ILHDFGIQSTRYLQVNYQDSQDWFI LVSVIADLRN AFYVLFP IWFHLK  
C1 MEKGM DVLHDFGIQSTHYLQVNYQDSQDWFI LVSVIADLRN AFYVLFP IWFHLR  
H1 MEEGM NVLHDFGIQSTHYLQVNYQDSQDWFI LVSVIADLRN AFYVLFP IWFHLQ

Hp QTVG TKMIWVAVIGDWLNLIFK WILFGHRPYWV VQETQIYPNHSSPCLEQFP TT  
Mp QNVG TKMIWVAVIGDWENLIFK WILFGHRPYWV IQETEIYPNHSSPCLEQFP TT  
F1 RDTALRLI WVAVIGDWLNLVLK WVLFGERP YWVWVHETKFGAGPAPSLQQFP IT  
M1 ETVG INLLWVAVVGDWENLVFK WILFGQRP YWVWVMDTDYYSNSSVP I IKQFP VT  
C1 EAVGI KLLWVAVIGDWLNLVFK WILFGQRP YWVWVMDTDYYSNTSVPLIKQFP VT  
H1 EAVGI KLLWVAVIGDWLNLVFK WILFGQRP YWVWVMDTDYYSNTSVPLIKQFP VT

Hp CETGPGSPSGHAMGASCVWYVMVTAALSH TVCGMDKFSITLHRLTWSFLWSVFW  
Mp CETGPGSPSGHAMGSSCVWYVMVTAALSYTISRMEESSVTLHRLTWSFLWSVFW  
F1 CETGPGSPSGHAMGAAGVYVMVTALLS--IAREKQC PPLL YRFLYIGLWMLMG  
M1 CETGPGSPSGHAMGAAGVYVMVTSTLA--IFRGKKKPT YGFRCLNVILWLGFW  
C1 CETGPGSPSGHAMGTAGVYVMVTSTLS--IFRGKRPT YRFRCLNILLWLGFW  
H1 CETGPGSPSGHAMGTAGVYVMVTSTLS--IFQGKIKPT YRFRCLNVILWLGFW

Fig. 6A

Hp LIQISVCISRVEFIATHFPHQVILGVIGGMLVAEAFEHTPGIQTASLGTYLKTNL  
Mp LIQISVCISRVEFIATHFPHQVILGVIGGMLVAEAFEHTPGVHMASLSVYLKTNV  
F1 LVELVVCISRVMMAAHFPHQVIAGITGTLVAEVVSKEKWIYSASLKKYFLITL  
M1 AVQLNVCLSRITYLAAHFPHQVVAGVLSGIAVAETESHIRGIYNASLRKYCLITI  
C1 AVQLNVCLSRITYLAAHFPHQVVAGVLSGIAVAETERHIQSIYNASLKKYFLITF  
H1 AVQLNVCLSRITYLAAHFPHQVVAGVLSGIAVTETESHISHIYNASLKKYFLITF

Hp FLFLFAVGFYLLLRVLNIDLLWSVPIAKKWCANPDWIIHIDTTPFAGLVRNLGVL  
Mp FLFLFALGFYLLLRLEFGIDLLWSVPIAKKWCANPDWIIHIDSTPFAGLVRNLGVL  
F1 FLTSFAVGIFYLLKALDLDLLWTMEKAQKWCIRPEWVHLD SAPFASLLRNMGSL  
M1 FLFGFALGFYLLLRKGLGVDDLWTLEKAKRWCERPEWVHLD TTPFASLFKNLGTL  
C1 FLFSFAIGFYLLLRKGLGVDDLWTLEKARRWCERPEWVHID TTPFASLLKNVGTL  
H1 FLFSFAIGFYLLLRKGLGVDDLWTLEKAQRWCEQPEWVHID TTPFASLLKNLGTL

Hp FGLGFAINSEMFLSCRGGNNYTL SFRLLCALTSLTILQLYHFLQIPTHEEHLF  
Mp FGLGFAINSEMFLRSCQGENGT KPSFRLLCALTSLTMQLYRFIKIPTHAEP LF  
F1 FGLGLGLHSPFYKTTKMRIMSA --PLRIGCIVISVSLHLHLLDGWTFSPENHMTF  
M1 LGLGLALNSSMYRKSCKGELS KSFPRFACIVASLVLLHLFDSLKPPSQVELIF  
C1 FGLGVTLNSSMYRESCKGKLSKWFPFRLS CIVVSLILLHLFDSLKPPSQTELIF  
H1 FGLGLALNSSMYRESCKGKLSKWL PFRLLSIVASLVLLHVFDSLKPPSQVELVF

Fig. 6B

Hp YVLSFCKSASIPLTVVAFIPYSV-HMLMKQSGKKSQ  
Mp YLLSFCKSASIPLMVVALIPYCV-HMLMRPGDKKTK  
Fl YALSEFGKSAVALLIPTTLVPWALSKIYPVKTEGKNL  
Ml YILSFCKSATVPFASVSLIPYCLARILG-QTHKKSL  
Cl YTLSFCKSAAVPLASVSLIPYCLARVFD-QPDKKSL  
Hl YVLSFCKSAVVPLASVSVIPYCLAQVLG-QPHKKSL

Fig. 6C